

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25
SEQUENCE LISTING

<110> Bayer CropScience GmbH

<120> Plants with increased activity of a Class 3 branching enzyme

<130> BCS 03-5005-PCT

<150> EP 03090324.9

<151> 2003-09-30

<160> 6

<170> PatentIn version 3.1

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<212> DNA

<213> Solanum tuberosum

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Ser Ala Thr Glu Gln Pro Pro Pro Gln Arg Arg Lys Gln Arg Pro Glu
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Lys Tyr Lys Gln Ser Glu Glu Glu Lys Gly Ile Asp Pro Val Gly Phe
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Glu Arg Tyr Lys Ser Leu Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg
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Ala Arg Tyr Cys Ala Leu Ile Gly Asp Phe Asn Gly Trp Ser Thr Thr
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 Trp Phe Ile Ile Leu Glu Asp Lys Leu Arg Glu Gly Glu Glu Pro Asp
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 Glu Glu Glu Leu Glu Ala Met Pro Asp Ala Ala Thr Arg Tyr Lys Thr
 260 265 270
 Trp Lys Glu Gln Gln Lys Lys Asp Pro Ala Ser Asn Leu Pro Ser Tyr
 275 280 285
 Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile Gly
 290 295 300
 Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile Ala
 305 310 315 320
 Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr
 325 330 335
 Met Pro Ala Leu Pro His Gly Ser Lys His Arg Val Tyr Phe Asn Thr
 340 345 350
 Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val Ile
 355 360 365
 Pro Asp Ala Asp Gly Met Ala Leu Ala Val His Trp Glu Pro Pro Pro
 370 375 380
 Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys Ser
 385 390 395 400
 Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro Lys
 405 410 415
 Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val Lys
 420 425 430

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Glu Ala Gly Tyr Asn Ala Thr Gln Ile Ile Gly Val Val Glu His Lys
 435 440 445

Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser
 450 455 460

Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu Ala
 465 470 475 480

His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr Ala
 485 490 495

Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp
 500 505 510

Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly Thr
 515 520 525

Arg Met Phe Lys Tyr Gly Asp Pro Asp Val Leu His Phe Leu Leu Ser
 530 535 540

Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His Phe
 545 550 555 560

His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser Phe
 565 570 575

Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala
 580 585 590

Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His Pro
 595 600 605

Asn Val Ile Thr Ile Ala Val Asp Ala Thr Leu Tyr Pro Gly Leu Cys
 610 615 620

Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu
 625 630 635 640

Ser Ala Ser Glu Met Trp Leu Ala Leu Leu Glu Asn Thr Pro Asp His
 645 650 655

Glu Trp Cys Met Ser Lys Ile Val Ser Thr Leu Val Gly Asp Arg Gln
 660 665 670

Asn Thr Asp Lys Met Leu Leu Tyr Ala Glu Asn His Asn Gln Ser Ile
 675 680 685

Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly
 690 695 700

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Lys Ser Ser Ile Ser Gln Glu Ser Leu Leu Arg Gly Cys Ser Leu His
 705 710 715 720
 Lys Met Ile Arg Leu Ile Thr Ser Thr Ile Gly Gly His Ala Tyr Leu
 725 730 735
 Asn phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe Pro
 740 745 750
 Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp
 755 760 765
 Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Ser Phe Asp Lys Asp
 770 775 780
 Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala
 785 790 795 800
 Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu Arg
 805 810 815
 Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr Glu
 820 825 830
 Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr Leu
 835 840 845
 Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His Asp
 850 855 860
 Gln Asn Thr Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg Phe
 865 870 875 880
 Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu
 885 890 895
 Thr Arg Ile Leu Arg Ala
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<211> 3047

<212> DNA

<213> Solanum tuberosum

<220>

<221> CDS

<222> (5)..(2710)

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act tgg aaa gag caa caa aaa gag gat ccg gca agc aat ttg cca tcg Thr Trp Lys Glu Gln Gln Lys Glu Asp Pro Ala Ser Asn Leu Pro Ser 275 280 285	865
tat gat gtg gta gat agt gga aaa gaa tat gat att tac aat att ata Tyr Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile 290 295 300	913
ggt gat cct gaa tcg ttt aag aaa ttt cgt atg aaa cag cct cct att Gly Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile 305 310 315	961
gct tac tgg tta gaa act aaa aag gga agg aaa ggc tgg tta cag aaa Ala Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys 320 325 330 335	1009
tat atg cct gct tta cct cat gga agc aaa tac agg gtg tat ttt aac Tyr Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn 340 345 350	1057
aca cca aat ggg cct ctt gaa cga gtt cct gcg tgg gcc aat ttt gtc Thr Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val 355 360 365	1105
att cca gat gca ggc ggg atg gca tta gca gtc cat tgg gaa cca cct Ile Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro 370 375 380	1153
cct gaa tat gct tat aaa tgg aaa cac aag cta cca gtc aag cct aag Pro Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys 385 390 395	1201
tcc ttg cgc ata tat gaa tgt cat gtt ggc atc tct ggc cag gaa cca Ser Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro 400 405 410 415	1249
aaa gtt tca tct ttc aat gat ttt att agc aag gtc ctt ccg cat gta Lys Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val 420 425 430	1297
aaa gaa gct gga tac aat gca ata caa att att gga gtt gtt gag cac Lys Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His 435 440 445	1345
aag gat tat ttc act gtt gga tat aga gtg acc aat ttt tat gct gtt Lys Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val 450 455 460	1393
agt agc cgt tat ggc aca ccg gat gac ttc aag cgc ttg gtt gat gaa Ser Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu 465 470 475	1441
gca cat ggg ctt gga ctg ctt gtc ttt ttg gag att gtg cac tct tat Ala His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr 480 485 490 495	1489
gca gca gca gat gaa atg gtt ggg tta tct ctt ttt gat gga gca aat Ala Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn 500 505 510	1537
gat tgc tat ttc cac act ggt aaa cgt gga cac cac aaa ttc tgg ggc Asp Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly 515 520 525	1585

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aca cgg atg ttc aaa tat gga gat ctt gat gtt ctg cac ttt ctt ctt	1633
Thr Arg Met Phe Lys Tyr Gly Asp Leu Asp Val Leu His Phe Leu Leu	
530 535 540	
tca aat ctg aac tgg tgg gtg gag gag tat cat gtc gat ggc ttc cat	1681
Ser Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His	
545 550 555	
ttt cat tcg ctc tcg tcc atg ttg tat acg cat aat gga ttt gct tca	1729
Phe His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser	
560 565 570 575	
ttt act ggt gac atg gat gaa tac tgt aac caa tat gtt gac aag gag	1777
Phe Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu	
580 585 590	
gcc tta ttg tac ctc ata tta gca aat gaa gta tta cat gct ctt cat	1825
Ala Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His	
595 600 605	
cct aat gtg atc acg att gct gag gat gca act ctg tat cct gga ctc	1873
Pro Asn Val Ile Thr Ile Ala Glu Asp Ala Thr Leu Tyr Pro Gly Leu	
610 615 620	
tgc gat cca aca tct caa ggt gga ctg ggc ttt gat tat ttt gcc aat	1921
Cys Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn	
625 630 635	
ctt tct gcc tca gag atg tgg ctt gca tta ctt gaa aat act cct gat	1969
Leu Ser Ala Ser Glu Met Trp Leu Ala Leu Leu Glu Asn Thr Pro Asp	
640 645 650 655	
cat gaa tgg tgc atg agt aag att gtt agc aca tta gtg ggc gat aga	2017
His Glu Trp Cys Met Ser Lys Ile Val Ser Thr Leu Val Gly Asp Arg	
660 665 670	
caa aat act gat aaa atg ctt ttg tat gca gaa aat cac aac cag tcc	2065
Gln Asn Thr Asp Lys Met Leu Leu Tyr Ala Glu Asn His Asn Gln Ser	
675 680 685	
att tct gga ggt cgt tcc ttc gca gaa ata ctg att ggt aac tcc ttg	2113
Ile Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu	
690 695 700	
ggg aaa tcc tcc ata tca caa gag tca tta ctt aga ggc tgc tcg tta	2161
Gly Lys Ser Ser Ile Ser Gln Glu Ser Leu Leu Arg Gly Cys Ser Leu	
705 710 715	
cac aag atg atc aga tta att aca tct aca att ggt ggt cat gca tac	2209
His Lys Met Ile Arg Leu Ile Thr Ser Thr Ile Gly Gly His Ala Tyr	
720 725 730 735	
ctc aac ttc atg ggc aat gaa ttt ggt cac cca aag aga gta gag ttt	2257
Leu Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe	
740 745 750	
cca atg tca agc aac aat ttc tcc ttt tca ctg gct aac cgt cgc tgg	2305
Pro Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp	
755 760 765	
gat cta ttg gaa gat gtt gta cat tat caa ttg ttc tca ttt gat aag	2353
Asp Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Phe Asp Lys	
770 775 780	
ggt atg atg gac ttg gat aaa aat ggg aga att ttg tcc aga ggt ctt	2401
Gly Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu	
785 790 795	

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gcc aac att cac cat gtc aat gat act acc atg gtg att tct tac ttg 2449
 Ala Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu 815
 800 805 810
 aga ggt ccc aat ctc ttt gtg ttc aac ttt cat cct gtc aat tca tat 2497
 Arg Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr 830
 820 825
 gaa aga tac att ata ggt gtg gaa gaa gct gga gag tat caa gtc aca 2545
 Glu Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr 845
 835 840
 tta aat aca gat gaa aac aag tat ggt ggt aga gga cta ctt ggc cat 2593
 Leu Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His 860
 850 855
 gat cag aat att caa aga acc att agt aga aga gct gat gga atg aga 2641
 Asp Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg 875
 865 870
 ttt tgc ttg gaa gtg cct ctg cca agt aga agt gct cag gtc tac aag 2689
 Phe Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys 895
 880 885 890
 ttg acc cga att cta aga gca tgatcactct agtaatcaaa gtgcctcata 2740
 Leu Thr Arg Ile Leu Arg Ala 900
 900
 tgatgacaca aaaggaaagg ttctacattg cccttacact gatcaatatt gacacctttc 2800
 cgagggtgagt ttctgtgatt cttgagcaga ctgttggtgcta gtcaattatc atgaactttt 2860
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 tggcttgtca tggggggtcat aagcatccgc cagattaaga tttcacaggc ctcgagtaaa 2980
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 taaagtg 3047
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 20 25 30
 Leu Lys Phe Val Arg Ser Arg Arg Ala Arg Val Ser Arg Cys Arg Cys
 35 40 45
 Ser Ala Thr Glu Gln Pro Pro Pro Gln Arg Arg Lys Gln Arg Pro Glu
 50 55 60

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Lys Tyr Lys Gln Ser Glu Glu Gly Lys Gly Ile Asp Pro Val Gly Phe
 65 70 75 80
 Leu Ser Lys Tyr Gly Ile Thr His Lys Ala Phe Ala Gln Phe Leu Arg
 85 90 95
 Glu Arg Tyr Lys Ser Leu Lys Asp Leu Lys Asp Glu Ile Leu Thr Arg
 100 105 110
 His Phe Ser Leu Lys Glu Met Ser Thr Gly Tyr Glu Leu Met Gly Met
 115 120 125
 His Arg Asn Ile Gln His Arg Val Asp Phe Leu Glu Trp Ala Pro Gly
 130 135 140
 Ala Arg Tyr Cys Ala Leu Ile Gly Asp Phe Asn Gly Trp Ser Thr Thr
 145 150 155 160
 Gly Asn Cys Ala Arg Glu Gly His Phe Gly His Asp Asp Tyr Gly Tyr
 165 170 175
 Trp Phe Ile Ile Leu Glu Asp Lys Leu Arg Glu Gly Glu Glu Pro Asp
 180 185 190
 Lys Leu Tyr Phe Gln Gln Tyr Asn Tyr Ala Glu Asp Tyr Gly Lys Gly
 195 200 205
 Asp Thr Gly Ile Thr Val Glu Glu Ile Phe Lys Lys Ala Asn Asp Glu
 210 215 220
 Tyr Trp Glu Pro Gly Glu Asp Arg Phe Ile Lys Ser Arg Tyr Glu Val
 225 230 235 240
 Ala Ala Lys Leu Tyr Glu Glu Met Phe Gly Pro Asn Gly Pro Gln Thr
 245 250 255
 Glu Glu Glu Leu Glu Ala Met Pro Asp Ala Ala Thr Arg Tyr Lys Thr
 260 265 270
 Trp Lys Glu Gln Gln Lys Glu Asp Pro Ala Ser Asn Leu Pro Ser Tyr
 275 280 285
 Asp Val Val Asp Ser Gly Lys Glu Tyr Asp Ile Tyr Asn Ile Ile Gly
 290 295 300
 Asp Pro Glu Ser Phe Lys Lys Phe Arg Met Lys Gln Pro Pro Ile Ala
 305 310 315 320
 Tyr Trp Leu Glu Thr Lys Lys Gly Arg Lys Gly Trp Leu Gln Lys Tyr
 325 330 335

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Met Pro Ala Leu Pro His Gly Ser Lys Tyr Arg Val Tyr Phe Asn Thr
 340 345 350
 Pro Asn Gly Pro Leu Glu Arg Val Pro Ala Trp Ala Asn Phe Val Ile
 355 360 365
 Pro Asp Ala Gly Gly Met Ala Leu Ala Val His Trp Glu Pro Pro Pro
 370 375 380
 Glu Tyr Ala Tyr Lys Trp Lys His Lys Leu Pro Val Lys Pro Lys Ser
 385 390 395 400
 Leu Arg Ile Tyr Glu Cys His Val Gly Ile Ser Gly Gln Glu Pro Lys
 405 410 415
 Val Ser Ser Phe Asn Asp Phe Ile Ser Lys Val Leu Pro His Val Lys
 420 425 430
 Glu Ala Gly Tyr Asn Ala Ile Gln Ile Ile Gly Val Val Glu His Lys
 435 440 445
 Asp Tyr Phe Thr Val Gly Tyr Arg Val Thr Asn Phe Tyr Ala Val Ser
 450 455 460
 Ser Arg Tyr Gly Thr Pro Asp Asp Phe Lys Arg Leu Val Asp Glu Ala
 465 470 475 480
 His Gly Leu Gly Leu Leu Val Phe Leu Glu Ile Val His Ser Tyr Ala
 485 490 495
 Ala Ala Asp Glu Met Val Gly Leu Ser Leu Phe Asp Gly Ala Asn Asp
 500 505 510
 Cys Tyr Phe His Thr Gly Lys Arg Gly His His Lys Phe Trp Gly Thr
 515 520 525
 Arg Met Phe Lys Tyr Gly Asp Leu Asp Val Leu His Phe Leu Leu Ser
 530 535 540
 Asn Leu Asn Trp Trp Val Glu Glu Tyr His Val Asp Gly Phe His Phe
 545 550 555 560
 His Ser Leu Ser Ser Met Leu Tyr Thr His Asn Gly Phe Ala Ser Phe
 565 570 575
 Thr Gly Asp Met Asp Glu Tyr Cys Asn Gln Tyr Val Asp Lys Glu Ala
 580 585 590
 Leu Leu Tyr Leu Ile Leu Ala Asn Glu Val Leu His Ala Leu His Pro
 595 600 605

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Asn Val Ile Thr Ile Ala Glu Asp Ala Thr Leu Tyr Pro Gly Leu Cys
 610 615 620
 Asp Pro Thr Ser Gln Gly Gly Leu Gly Phe Asp Tyr Phe Ala Asn Leu
 625 630 635 640
 Ser Ala Ser Glu Met Trp Leu Ala Leu Leu Glu Asn Thr Pro Asp His
 645 650 655
 Glu Trp Cys Met Ser Lys Ile Val Ser Thr Leu Val Gly Asp Arg Gln
 660 665 670
 Asn Thr Asp Lys Met Leu Leu Tyr Ala Glu Asn His Asn Gln Ser Ile
 675 680 685
 Ser Gly Gly Arg Ser Phe Ala Glu Ile Leu Ile Gly Asn Ser Leu Gly
 690 695 700
 Lys Ser Ser Ile Ser Gln Glu Ser Leu Leu Arg Gly Cys Ser Leu His
 705 710 715 720
 Lys Met Ile Arg Leu Ile Thr Ser Thr Ile Gly Gly His Ala Tyr Leu
 725 730 735
 Asn Phe Met Gly Asn Glu Phe Gly His Pro Lys Arg Val Glu Phe Pro
 740 745 750
 Met Ser Ser Asn Asn Phe Ser Phe Ser Leu Ala Asn Arg Arg Trp Asp
 755 760 765
 Leu Leu Glu Asp Val Val His Tyr Gln Leu Phe Ser Phe Asp Lys Gly
 770 775 780
 Met Met Asp Leu Asp Lys Asn Gly Arg Ile Leu Ser Arg Gly Leu Ala
 785 790 795 800
 Asn Ile His His Val Asn Asp Thr Thr Met Val Ile Ser Tyr Leu Arg
 805 810 815
 Gly Pro Asn Leu Phe Val Phe Asn Phe His Pro Val Asn Ser Tyr Glu
 820 825 830
 Arg Tyr Ile Ile Gly Val Glu Glu Ala Gly Glu Tyr Gln Val Thr Leu
 835 840 845
 Asn Thr Asp Glu Asn Lys Tyr Gly Gly Arg Gly Leu Leu Gly His Asp
 850 855 860
 Gln Asn Ile Gln Arg Thr Ile Ser Arg Arg Ala Asp Gly Met Arg Phe
 865 870 875 880

BCS 03-5005_PCT-SEQUENZPROTOKOLL.ST25

Cys Leu Glu Val Pro Leu Pro Ser Arg Ser Ala Gln Val Tyr Lys Leu
885 890 895

Thr Arg Ile Leu Arg Ala
900